

SEQUENCE PROTOCOL

<110> Degussa AG

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<130> 000557 BT

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<170> PatentIn Ver. 2.1

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<213> Corynebacterium glutamicum

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<222> (259) .. (2130)

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tctgaggacg cgcactctgc agatgcagac aacgcgagca atgtaatcaa tgagaatgag 180

gactcctcgg aagggtgctaa ccagccttca aacgagtcac cctctacgga agccaaatcc 240

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ggcttcgatg cactcgga ctg cca gag cgt gta ctt gac gct gtg cgc aag 291

Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys
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gtg ggt tac gaa act cct tcc cca att cag gca caa acc atc cca atc 339
Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile
15 20 25

45

ctc atg gag ggc cag gat gtt gtt ggt cta gca cag acc ggt acc ggt 387
Leu Met Glu Gly Gln Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly
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aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac aag tcc 435
Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser
45 50 55gtg cgc agc cca cag gca ctt gtg ctt gcc cct acc cgt gag cag gca 483
Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala
60 65 70 75

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ctt cag gtt gct gac tcc ttc caa tcc ttc gct gac cac gtc ggt ggc 531
Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly
80 85 90

ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att cag ctc 579
 Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu
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5 tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca ggc cga 627
 Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro Gly Arg
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10 atc atc gat cac ctc gaa aag ggc tcc ctg gat atc tcc gga ctg cgc 675
 Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg
 125 130 135

15 ttc ctc gtg ctc gat gaa gca gac gag atg ctg aac atg ggc ttc cag 723
 Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln
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20 gaa gat gtc gag cgc atc ctc gag gac acc cca gac gag aag cag gtt 771
 Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val
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gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg tcc aag 819
 Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys
 175 180 185

25 cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag acc agg 867
 Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg
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30 act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac cgc aac 915
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35 aag atg gat gca ctg acc cgt att ctc gag gtc acc gag ttt gaa gca 963
 Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala
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40 atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt gct gaa 1011
 Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu
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45 gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac ggc cgc 1107
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50 ctg gac atc ctc gtt gca acc gac gtt gca gcc cgt ggt ctt gac gtt 1155
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55 gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac acc gag 1203
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 Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly
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 15 acc aag tcc ctc gag gac aag cag atg gac ctg ttc cgc acc ctg gtc 1443
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 50 cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc ggc cag 1875
 Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln
 525 530 535
 55 ctc atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc cgc ttc 1923
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5 gac cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc cgt gga 2019
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 575 580 585

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15 ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc ggt tac 2115
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20 cgt ggc gga cgc gac taagagttcg ttttagcttc agctcaggtt ttcgcctgag 2170
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45 Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln
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Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro
 85 90 95

55 Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg
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Gly Ala His Ile Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu
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Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp
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 10 Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn
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 Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile
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 15 Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu
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 20 Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val
 225 230 235 240
 Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg
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 25 Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg
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 275 280 285
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 325 330 335
 40 Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser Ile Glu Arg Ala Thr
 340 345 350
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 355 360 365
 45 Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu
 370 375 380
 Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln
 385 390 395 400
 Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln
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 55 Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg
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